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EMBOSS Align Results

Needle Results	
Matrix	DNAfull
Open gap penalty	10.0
Gap extension penalty	0.5
Needle output	needle-20110228-0453413765.output

SUBMIT ANOTHER JOB

```
##########################################
# Program: needle
# Rundate: Mon 28 Feb 2011 04:53:41
# Commandline: needle
#    [-asequence] /ebi/extserv/old-work/needle-20110228-0453413765.input.1
#    [-bsequence] /ebi/extserv/old-work/needle-20110228-0453413765.input.2
#    -outfile /ebi/extserv/old-work/needle-20110228-0453413765.output
#    -gapopen 10.0
#    -gapextend 0.5
#    -datafile EDNAFULL
#    -sprotein1
#    -sprotein2
#    -auto
# Align_format: srspair
# Report_file: /ebi/extserv/old-work/needle-20110228-0453413765.output
##########################################

#=======================================
#
# Aligned_sequences: 2
# 1: EMBOSS_001
# 2: EMBOSS_001
# Matrix: EDNAFULL
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1180
# Identity:     771/1180 (65.3%)
# Similarity:   771/1180 (65.3%)
# Gaps:         179/1180 (15.2%)
# Score: 2517.0
#
#
#=======================================
```

```
DNA encoding A26054   EMBOSS_001      1 atggaaagatg-gtttaaa------tct-ctgtttgttct----------    32
                                        ||| .|.|.||        ||| ||||.||..||
        SEQ ID NO:2   EMBOSS_001      1 --------ATGCCTCTCAAGCCGATTCTCCTGTCTGCCCTGGCCAGTCTC    42

                      EMBOSS_001     33 ----------------tgttttatt-------------------ttttgt    47
                                                        ||.|.||.|                .||.||
                      EMBOSS_001     43 GCCTCGGCCTCTCCGCTGCTCTACTCGCGGACCACCAATGAAACCTTCGT    92

                      EMBOSS_001     48 ttttac----------ggcctc-----------ggcggccgacaagctgc    76
                                        .||.||          ||||||           |..|..|..||..||||
                      EMBOSS_001     93 CTTCACCAATGCCAATGGCCTCAACTTCACCCAGATGAACACCACCCTGC    142

                      EMBOSS_001     77 cgaacatagtcattctcgcaacgggtggtaccatcgcgggctccgctgcc    126
                                        |||||.|.|...|||| .|||||||||||||||||||||||||||.|.||
                      EMBOSS_001    143 CGAACGTGACCATTTTCGCAACGGGTGGTACCATCGCGGGCTCCGATTCC    192

                      EMBOSS_001    127 accggaacccagacgaccggctacaaggaccggagcactcagggtcgatac    176
```

```
EMBOSS_001       177 cctcatcaatgcggtgccagaggtgaagaaactggccaatgttaagggcg      226
                     ||||||||.||||||||||||||....||..|.|..||||||||||||...||||
EMBOSS_001       243 CCTCATCGATGCGGTGCCATCCATGCTGGATGTGGCCAATGTTGCCGGCG      292

EMBOSS_001       227 agcagttctccaacatggccagcgagaacatgaccggtgacgtggtgctt      276
                     ..|||.|..|||||.|||..||||||.||.||.||||..||||.|..||.||
EMBOSS_001       293 TCCAGGTGGCCAACGTGGGAAGCGAGGATATCACCTCTGACATCCTGATT      342

EMBOSS_001       277 aagctgtcccagcgggtgaacgagc------tgctagcacgggacgatgt      320
                     ....|||||.||..|.|||.|.|| ||        ||..||.||..|||.| |
EMBOSS_001       343 TCCATGTCCAAGAAGCTGAAC-CGCGTTGTATGTGAGGACCCGACCA--T      389

EMBOSS_001       321 ggacggtgttgtcatcacccacggcaccgacaccgtggaggagtctgcct      370
                     ||.|||||.||||||||||||||||||||||||||.|.||||||.|||||||
EMBOSS_001       390 GGCCGGTGCTGTCATCACCCACGGCACCGACACCCTCGAGGAGACTGCCT      439

EMBOSS_001       371 acttcctgcacctcactgtcaaaagtgacaagccagttgtctttgtggct      420
                     .|||||||.||..|||||||||...|||.||||||.|||||.|.|||||.|
EMBOSS_001       440 TCTTCCTGGACGCCACTGTCAACTGTGGCAAGCCAATTGTCATCGTGGGT      489

EMBOSS_001       421 gccatgcgcccagccacggccatctcagctgacgggcccatgaatctgct      470
                     |||||||||||||.||||||||||||||||||||||||||||.|.||||||||
EMBOSS_001       490 GCCATGCGCCCATCCACGGCCATCTCAGCTGACGGGCCCTTCAATCTGCT      539

EMBOSS_001       471 cgaagccgtgcgggtggctggcgacaagcagtcgcgcggtcgcggtgtca      520
                     |||||||||||..|||||||||.|..||.|..|.|||||||.|||||||.||
EMBOSS_001       540 CGAAGCCGTGACGGTGGCTGCCTCCACGTCGGCGCGCGATCGCGGTGCCA      589

EMBOSS_001       521 tggtggtcctcaacgatcgcattggctcggcccgctatatcaccaagacc      570
                     |||||||.|.|.||||||||||||||||.||||||||..||||.|.||||||||
EMBOSS_001       590 TGGTGGTCATGAACGATCGCATTGCCTCGGCCTACTATGTGACCAAGACC      639

EMBOSS_001       571 aatgcctccactctggacaccttcaaggccaatgaggagggctaccttgg      620
                     ||||||..|||||.|||||||||||||||||||||||..|||..||||||||||
EMBOSS_001       640 AATGCCAACACTATGGACACCTTCAAGGCCATGGAGATGGGCTACCTTGG      689

EMBOSS_001       621 cgtgatcatcggcaac-cgcatt-----tactaccaaaaccgtatcgaca      664
                     ||.|||.|||..|||| |.|.||    |.||||       |||  ..||.||
EMBOSS_001       690 CGAGATGATCTCCAACACCCCTTTCTTCTTCTAC-----CCG-CCCGTCA      733

EMBOSS_001       665 agctgcataccactcggt----cggtctttgacgtccgcggcctgacttc      710
                     ||          |||..||||    .||.|||||.||.||||.||..|||..
EMBOSS_001       734 AG-------CCAACCGGTAAGGTGGCCTTTGACATCACCAACGTGACTGA      776

EMBOSS_001       711 gctccccaaagtggacattctgtatggttatcaggac---gaccccgaat      757
                     |.|||||...||.||||||||||.||.||||.|||||   .||..||||..
EMBOSS_001       777 GATCCCCCGTGTGGACATTCTGTTTTCTTATGAGGACATGCACAACGACA      826

EMBOSS_001       758 acctctacgacgccgccatccagcatggtgtcaagggaattgtgtatgcc      807
                     .||||||||.|||||..| ||||| ||||||.|.||||||||||.||||||
EMBOSS_001       827 CCCTCTACAACGCCATC-TCCAG--TGGTGCCCAGGGAATTGTGATTGCC      873

EMBOSS_001       808 gggatgggtgctggatccgtctca-----gttc---gtgg-tat------      842
                     |||...||||||||||.|||||.|| .|||   |.||  |||
EMBOSS_001       874 GGGGCTGGTGCTGGAGGCGTCACAACCTCCTTCAATGAGGCTATCGAGGA      923

EMBOSS_001       843 tgccggcatgcgtaaggctatggagaaaggggtcgttgtcatacggagta      892
                     ||.|..||..||       |.|||||||       ||..||||.|.|.||||||
EMBOSS_001       924 TGTCATCAACCG------TTTGGAGA------TCCCTGTCGTGCAGAGTA      961

EMBOSS_001       893 cgcgcacaggcaatgggatagtgccac---ccgac--gaagagctccccg      937
                     .|||||||.||||||||..||||||||   |.|||| ||..|||..|.|.
EMBOSS_001       962 TGCGCACAGTCAATGGGGAAGTGCCACTGTCAGACGTGAGCAGCGACACC      1011

EMBOSS_001       938 gcc-------tcgtcagtgactccctaaacccggcgcatgcccgcattct      980
                     |||          |||.|||||..|.|||||||||||..|.|..|||||||||
EMBOSS_001      1012 GCCACCCACATCGCCAGTGGATACCTAAACCCGCAGAAGTCCCGCATTCT      1061

DNA encoding A26054    EMBOSS_001       981 gttgatgttggcgctaactc--ggacaag--tgatcctaaagtaatccaa      1026
                                           ||||...|||..|||||.|.|   ||| ||||  .|.|.||||...
```

```
                                      ||  ||.|||.|          ||.||||.
  SEQ ID NO:2  EMBOSS_001   1108 GACGTGTTTGCTCTGGGCACGGATGCGTAG   1137


              #-------------------------------------
              #-------------------------------------
```